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Oct 4 2004 14:35:49



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                 complement (31719...31830)
exon
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gene
                 complement(join(35411..36565,36894..37147,38153..38288,
                 38378..38518,38602..38855,38904..39290,39384..39561))
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CDS
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                 38378..38518,38602..38855,38904..39290,39384..39561))
                /gene="dl3030c"
                /note="similarity to heat shock transcription factor HSF30
                Contains HSF-type DNA-binding domain signature
                 [LPTYFKHNNFSSFIRQLNTYGFRKI]"
                /codon start=1
                /product="heat shock transcription factor like protein"
                /protein id="CAB10177.1"
                /db xref="G1:2244754"
                /db xref="GOA:023259"
                /db_xref="UniProt/TrEMBL:023259"
                translation="MEEDRESRVSAKPSGDRVDRLRNLPDCLLFKILLNLPTKDVVKL/
                SVLSRRWRNVWRYVPGFNSESCLQKFKLTVNWYDDVQLETVHFTEWFNAVVKRKVQHL
                HILDKTWGRDEVVIPPTVFTCGSLISLNLYDVYLPNREFVSLPSLKVIVLDAVVFDED
                FAFEMLVSGCPVLESLSVNKINLNDISENDDDYLEVVIDAPRLHYLKLNDKRTASFIM
                KNHGSLLKADIDFVFNLGSEYMFDPNYLPTRHIIRDFLVGLSGVKDMIISSSTLQVIY
                DYSRCEQLPLFRNVSFLRVEFADYRWEMLPIFLESCPNLKSLVLGFSIPPGKEGANIL
                PGPRRFLTSLEYVKIAKPMAAEASEIKLKLVNSTMNGALGNSSASVSGGEGAGGPAPF
                LVKTYEMVDDSSTDQIVSWSANNNSFIVWNHAEFSRLLLPTYFKHNNFSSFIRQLNTY
                GFRKIDPERWEFLNDDFIKDQKHLLKNIHRRKPIHSHSHPPASSTDQERAVLQEQMDK
                LSREKAAIEAKLLKFKQQKVVAKHQFEEMTEHVDDMENRQKKLLNFLETAIRNPTFVK
                NFGKKVEQLDISAYNKKRRLPEVEQSKPPSEDSHLDNSSGSSRRESGNIFHQNFSNKL
                RLELSPADSDMNMVSHSIQSSNEEGASPKGILSGGDPNTTLTKREGLPFAPEALELAD
                TGTCPRRLLLNDNTRVETLQQRLTSSEETDGSFSCHLNLTLASAPLPDKTASQIAKTT
                LKSQELNFNSIETSASEKNRGRQE1AVGGSQANAAPPARVNDVFWEQFLTERPGSSDN
                EEASSTYRGNPYEEQEEKRNGSMMLRNTKNIEQLTL"
                complement (35411..36565)
exon
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intron
                complement (36566..36893)
                /gene="dl3030c"
                /number=1
                complement (36894..37147)
exon
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                 /gene="dl3030c"
                 /number=2
                 complement (38153..38288)
exon
                 /gene="d13030c"
                 /number=3
                 complement (38289...38377)
intron
                 /qene="d13030c"
                 /number=3
                 complement (38378..38518)
exon
                 /gene="d13030c"
                 /number=4
intron
                complement (38519..38601)
                 /gene="d13030c"
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exon
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                complement (38856..38903)
intron
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                 /number=5
exon
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intron
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                /gene="d13030c"
                /number=6
                complement (39384..39561)
exon
                /gene="dl3030c"
                /number=7
                42311..43852
gene
                /gene="d13035w"
CDS
                join(42311..42901,42950..43406,43452..43852)
                /gene="dl3035w"
                /note="weak similarity to cytochrome P450, human"
                /codon start=1
                /product="hypothetical protein"
                /protein id="CAB10178.1"
                /db xref="GI:2244755"
                /db_xref="GOA:023260"
                /db xref="UniProt/TrEMBL:023260"
                /translation="MEKPISITTGKFRTNNNNHNNVWFVVPLFFILCFVLLCFDYSA
                LFTDTDETAFSIPDVTQKSTSSEFTKDDNFSRFPDDPSPDSSCSGRYIYVHELPYRFN
                GDLLDNCFKITRGTEKDICPYIENYGFGPVIKNYENVLLKQSWFTTNQFMLEVIFHNK
                MINYRCLTNDSSLASAVFVPFYAGLDMSRYLWGFNITKEWGRMSGRDHFLVSGRIAWD
                FRRQTDNESDWGSKLRFLPESRNMSMLSIESSSWKNDYAIPYPTCFHPRSVDEIVEWO
                ELMRSRKREYLFTFAGAPRPEYKDSVRGKIIDECLESKKQCYLLDCNYGNVNCDNPVN
                VMKVFRNSVFCLQPPGCIPVFFHPGTAYAQYKWHLPKNHSSYSVYLPVKDVKEWNIKI
                KERLIEIPEERVVRLREEVIRLIPKVVYADPKYGSDGSEDAFELAVKGMLERIEEVRE
                MMRQGKDGSDGFDDRDDYKYTFSPYEEPOVLA"
                42311..42901
exon
                /gene="d13035w"
                /number=1
                42902..42949
intron
                /gene="dl3035w"
                /number=1
                42950..43406
exon
                /gene="d13035w"
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                 43407..43451
                 /gene="d13035w"
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exon
                 43452..43852
                 /gene="dl3035w"
                 /number=3
                 48743..50124
gene
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CDS
                 join(48743..48871,48963..49025,49109..49175,49264..49364,
                 49454..49498, 49582..49620, 49672..49863, 49951..50124)
                 /gene="dl3040w"
                 /note="similar to K01A11.2 - Caenorhabditis elegans"
                 /codon start=1
                 /product="hypothetical protein"
                 /protein_id="CAB10179.1"
                 /db_xref="GI:2244756"
                 /db xref="UniProt/TrEMBL:023261"
                 translation="MATKPTFQLFSSSQGSGLGLGFLDSSEPALPPPPPPPVEVLSFEV/
                 SSSTDFEVDKLTIGEITLLKGRVSTKEVFGLPNSDLVPGVYEGGLKLWEGSIDLVKAL
                 EKESQTGNLSFSGKRVLELGCGHALPGIYACLKGSDAVHFQDFNAESSSVSVSETEVR
                 FFAGEWSEVHQVLPLVNSDGETNKKGGYDIILMAETIYSISAQKSQYELIKRCLAYPD
                 GAVYMAAKKYYFGVGGGTRQFLSMIEKDGKMVYSMMYIKQQLHCSFSTMII"
exon
                 48743..48871
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                 /number=1
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                 /number=2
intron
                 49026..49108
                 /gene="d13040w"
                 /number=2
                 49109..49175
exon
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                 /number=3
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                 /number=5
                 49582..49620
exon
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intron
                 49621..49671
                /gene="dl3040w"
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exon
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intron
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exon
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                 /number=8
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gene
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gene
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CDS
                 complement (50902..51255)
                 /gene="d13045c"
                 /note="predicted"
                 /codon start=1
                 /product="hypothetical protein"
                 /protein_id="CAB10180.1"
                 /db xref="GI:2244757"
                 /db xref="UniProt/TrEMBL:023262"
                translation="MEIKPSRIFSTITIFFLCLLLAHVTSKASSSSLCNGSVAECSSM/
                VETEEMSVIMESWSSQRLTEEQAHKLSYGALRRNQPACDGGKRGESYSTQCLPPPSNP
                YSRGCSKHYRCGRDS"
                complement (50902..51255)
exon
                /gene="d13045c"
                /number=1
                53262..53597
gene
                /gene="d13050c"
                complement (53262..53597)
gene
                /gene="d13050c"
                complement (53262..53597)
CDS
                /gene="d13050c"
                /note="predicted
                contains EST gb:716565"
                /codon start=1
                /product="hypothetical protein"
                /protein id="CAB10181.1"
                /db xref="GI:2244758"
                /db xref="UniProt/TrEMBL:023263"
                translation="MEYYTFTENDEERVSRNHHVNNTWVKERYESDEEDGEVNKLILK/
                EDEETKDMVTSPSGERMMLTSKVRYLTYGALKHDTAASAASGGGGRALPHPSNKYNRG
                HPKYYRCRG"
                complement (53262..53597)
exon
                /gene="d13050c"
                /number=1
                56013..58057
gene
                /gene="dl3055c"
                complement(join(56013..56294,56381..56653,56745..56852,
gene
                56957..57188,57271..57498,57589..57784,57904..58057))
                /gene="d13055c"
CDS
                complement(join(56013..56294,56381..56653,56745..56852,
                56957..57188,57271..57498,57589..57784,57904..58057))
                /gene="d13055c"
                /note="strong similarity to selenium-binding protein,
                hepatic, mouse
                contains EST qb:416465"
                /codon start=1
                /product="selenium-binding protein like"
                /protein_id="CAB10182.1"
                /db_xref="GI:2244759"
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/db xref="UniProt/Swiss-Prot:023264"
                 translation="MATETEVVAPVTVSNGGSKGCCKYGGPGYATPLAAMSGPSEKLI"
                 YVTAVYTGTGIDKPDYLATVDVDPSSPSYSSVIHRLPMPFVGDELHHSGWNSCSSCHG
                 DASVDRRYLVLPSLISGRIYAIDTKENPRAPSLYKYVDPKEIADKTGLAFPHTAHCLA
                 TGEILVSCLGDEEGNAKGNGFLLLDSDFNIKNRWEKPGHSPLYGYDFWYQPRHKTMIS
                 TSWGAPKAFSKGFNLQHVADGLYGSHLHVYSWPGGEIKQLIDLGPTGLLPLEIRFLHD
                 PSKDTGFVGSALSSNMIRFFKNSDETWSHEVVISVKPLKVENWILPEMPGLITDFLIS
                 LDDRFIYFVNWLHGDIRQYNIEDPKNPVLTGQIWVGGLLQKGSPVKAVGEDGNTFQFE
                 VPQIKGKSLRGGPQMIQLSLDGKRLYATNSLFSAWDRQFYPEIMEKGSHIIQIDVDTE
                 KGGLTINPDFFVDFGDEPDGPSLAHEMRYPGGDCTSDIWI"
exon
                 complement (56013..56294)
                 /gene="d13055c"
                 /number=1
intron
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                 /gene="d13055c"
                 /number=1
exon
                 complement (56381..56653)
                 /gene="d13055c"
                 /number=2
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intron
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                complement (56745..56852)
exon
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intron
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                /number=3
exon
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                /number=4
intron
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                complement (57271..57498)
exon
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                complement (57499..57588)
intron
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                complement (57589..57784)
exon
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                complement (57785..57903)
intron
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                /number=6
                complement (57904..58057)
exon
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gene
                /gene="d13061c"
gene
                complement(join(58583..58864,58952..59196,59303..59446,
                59538..59962,60043..60238,60576..60720))
                /gene="dl3061c"
CDS
                complement(join(58583..58864,58952..59196,59303..59446,
                59538..59962,60043..60238,60576..60720))
                /gene="dl3061c"
                /note="a non-consensus splicing site was generated
                strong similarity to selenium-binding protein, hepatic,
                mouse"
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/codon start=1
                 /product="selenium-binding protein like"
                 /protein id="CAB46000.1"
                 /db xref="GI:5280986"
                /db xref="GOA:023265"
                /db xref="UniProt/TrEMBL:023265"
                translation="MATETVLATAVSNGKSKGCCKSGPGYATPLAAMAGPREKLIYVT/
                ALYSGTGRDKPDYLATVDVDPSSPTFSSVIHRLKMPYIGDELHHTGWNSCSSCHGDAS
                ADRRYLVLPGLISGRIYAIDTKTDPKAPSLYKVVEPKEIAEKTGLAFPHTSHCLASGD
                MLVSCLGDKEGNAKGNGFLLLDSDFNVKSRWDKPGHGPLFGYDFWYQPRFKTMISTSW
                GAPKAFSKGFNLQHVADGLYGSHLHIYQWPEGEMKQITYWVFVVMWLQIRFLHDPSKD
                TGYVGSALSSNMIRFFKNSDDTWSHEAIENWILPEMPGLITDFLISLDDRFFYFVNWL
                HGDIRQYNIEDPKNPVLTGQIWVGGLLQKGSPYKAVGEDGNTYQFDVPQIKGKSLRAG
                PQMIQLSLDGKRLYATNSLFSAWDRQFYPEIMEKGSHIIQIDVDTDKGGLTLNPDFFV
                DFGDEPDGPALAHEMRYPGGDCTSDIWI"
                complement (58583..58864)
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                /gene="d13061c"
                /number=1
                complement (58952..59196)
exon
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                /number=2
                complement (59197..59302)
intron
                /gene="d13061c"
                /number=2
                complement (59303..59446)
exon
                /gene="d13061c"
                /number=3
                complement (59447..59537)
intron
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                /number=3
                complement (59538..59962)
exon
                /gene="dl3061c"
                /number=4
                complement (59963..60042)
intron
                /gene="d13061c"
                /number=4
                complement (60043..60238)
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                /number=5
                complement(60239..60575)
intron
                /gene="d13061c"
                /number=5
                complement (60576..60720)
exon
                /gene="dl3061c"
                /number=6
                61404..65452
gene
                /gene="d13066c"
                complement(join(61404..61467,61541..62548,62591..63331,
gene
                64429..64583,65360..65452))
                /gene="d13066c"
CDS
                complement(join(61404..61467,61541..62548,62591..63331,
                64429...64583,65360...65452))
                /gene="d13066c"
                /note="similar to hypothetical protein - Arabidopsis
                thaliana"
                /codon start=1
                /product="hypothetical protein"
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/protein_id="CAB46001.1"
                 /db xref="GI:5280987"
                 /db xref="UniProt/TrEMBL:023266"
                 translation="MGVPFAVVDGDTLDVVADGVGEKVVLIPPPLVELISSIIFLKKL/
                NGFRKSIVVRRKKLLFSLTFIFMFKLFVFFDFGSYFSRMNRTLTTAKALHAHIVKLGI
                VQCCPLANTLVNVYGKCGAASHALQVFDEMPHRDHIAWASVLTALNQANLSGKTLSVF
                SSVGSSSGLRPDDFVFSALVKACANLGSIDHGRQVHCHFIVSEYANDEVVKSSLVDMY
                AKCGLLNSAKAVFDSIRVKNTISWTAMVSGYAKSGRKEEALELFRILPVKNLYSWTAL
                ISGFVQSGKGLEAFSVFTEMRRERVDILDPLVLSSIVGACANLAASIAGRQVHGNALI
                DMYAKCSDVIAAKDIFSRMRHRDVVSWTSLIVGMAQHGQAEKALALYDDMVSHGVKPN
                EVTFVGLIYACSHVGFVEKGRELFQSMTKDYGIRPSLQHYTCLLDLLGRSGLLDEAEN
                LIHTMPFPPDEPTWAALLSACKRQGRGQMGIRIADHLVSSFKLKDPSTYILLSNIYAS
                ASLWGKVSEARRKLGEMEVRKDPGHSSVEVRKETEVFYAGETSHPLKEDIFRLLKKLE
                EEMRIRNGYVPDTSWILHDMDEQEKEKLLFWHSERSAVAYGLLKAVPGTPIRIVKNLR
                VCGDCHVVLKHISEITEREIIVRDATRYHHFKGGKCSCNDFCNYGHAKSIFILNKETI
                KWVS"
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                complement (61468..61540)
                /gene="d13066c"
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                complement (61541..62548)
exon
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intron
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                complement (62591..63331)
exon
                /gene="d13066c"
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                complement (63332..64428)
intron
                /gene="dl3066c"
                /number=3
                complement (64429...64583)
exon
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                /number=4
                complement (64584..65359)
intron
                /gene="d13066c"
                /number=4
                65297..66050
gene
                /gene="dl3070w"
CDS
                join(65297..65483,65782..66050)
                /gene="dl3070w"
                /note="strong similarity to major latex protein type 1,
                Arabidopsis thaliana
                contains EST gb:948081"
                /codon start=1
                /product="major latex protein like"
                /protein_id="CAB10185.1"
                /db xref="GI:2244762"
                /db xref="UniProt/TrEMBL:023267"
                translation="MATSGTYVTEVPLKGSAEKHYKRWRNENHLFPDAIGHHIQGVTV/
                HDGEWDSHGALKIWNYTLDGKPEMFKERREIDDENMAVTFVGLEGHVMEOLKVYDTIL
                QFIQKSPDDIVCKITMTWEKRADDSPEPSNYMKLVKSLAADMDAHVLKA"
exon
                65297..65483
                /gene="d13070w"
                /number=1
                complement (65360..65452)
exon
                /gene="d13066c"
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intron
                /gene="d13070w"
                /number=1
                65782..66050
exon
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                /number=2
                70014..75877
gene
                /gene="d13075c"
                complement(join(70014..70106,70202..70259,70335..70450,
gene
                70549..70628,70728..70887,71046..71183,71517..71597,
                71699..71752,71835..71993,72105..72210,72334..72401,
                72608..72757,72891..73006,73078..73286,73740..73812,
                74410..74524,75126..75311,75743..75877))
                /gene="d13075c"
                complement(join(70014..70106,70202..70259,70335..70450,
CDS
                70549..70628,70728..70887,71046..71183,71517..71597,
                71699...71752,71835...71993,72105...72210,72334...72401,
                72608..72757,72891..73006,73078..73286,73740..73812,
                74410..74524,75126..75311,75743..75877))
                /gene="d13075c"
                /note="strong similarity to AMP-binding protein - Brassica
                napus"
                /codon start=1
                /product="AMP-binding protein"
                /protein_id="CAB10186.1"
                /db xref="GI:2244763"
                /db xref="GOA:023268"
                /db xref="UniProt/TrEMBL:023268"
                /translation="MASTSSLGPSTLLSYGSPSRQFPDFGFRLISGHESVRIPSFRRF
                REKEVKPSSPFLESSSFSGDAALRSSEWKAVPDIWRSSAEKYGDRVALVDPYHDPPLK
                LTYKQLEQEILDFAEGLRVLGVKADEKIALFADNSCRWLVSDQGAVNVVRGSRSSVEE
                LLQIYRHSESVAIVVDNPEFFNRIAESFTSKASLRFLILLWGEKSSLVTQGMQIPVYS
                YAEIINQGQESRAKLSASNDTRSYRNQFIDSDDTAAIMYTSGTTGNPKGVMLTHRNLL
                HQIKHLSKYVPAQAGDKFLSMLPSWHAYERASEYFIFTCGVEQMYTSIRYLKDDLKRY
                QPNYIVSVPLVYETLYSGIQKQISASSAGRKFLALTLIKVSMAYMEMKRIYEGMCLTK
                EQKPPMYIVAFVDWLWARVIAALLWPLHMLAKKLIYKKIHSSIGISKAGISGGGSLPI
                HVDKFFEAIGVILQNGYGLTETSPVVCARTLSCNVLGSAGHPMHGTEFKIVDPETNNV
                LPPGSKGIIKVRGPQVMKGYYKNPSTTKQVLNESGWFNTGDTGWIAPHHSKGRSRHCG
                GVIVLEGRAKDTIVLSTGENVEPLEIEEAAMRSRVIEQIVVIGODRRRLGAIIIPNKE
                EAQRVDPETSKETLKSLVYQELRKWTSECSFQVGPVLIVDDPFTIDNGLMTPTMKIRR
                DMVVAKYKEEIDQLYS"
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exon
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                /number=1
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intron
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                /number=1
                complement (70202..70259)
exon
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                /number=2
                complement (70260..70334)
intron
                /gene="d13075c"
                /number=2
                complement (70335...70450)
exon
                /gene="d13075c"
                /number=3
intron
                complement (70451...70548)
                /gene="d13075c"
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                GFSKGAQNGFQSSGVDRFLLPASECEYTLDLLLDELQSDQWPVQPGHRPQRCTGVALS
                VAAGLLGACLPGTGARIVALVGGPCTEGPGTIISKDLSDPVRSHKDLDKDAAPYYKKA
                VKFYDSIAKQLVAQGHVLDLFASALDQVGVAEMKVAVESTGGLVVLSESFGHSVFKDS
                FKRMFEDGEHSLGLCFNGTLEINCSKDIKIQGVIGPCSSLEKKGPNVADTVIGEGNTS
                {\tt AWKLCGLDKSTCLTVFFDLSSTGSTAPGALNQQLYLQFITRYQNSEGKSLARVTTLTR}
                QWVDTAVSTENLVQGFDQETAAVVMARLTSLKMETEEGFDATRWLDRTLIRLCSKFGE
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                MIQPSLTSYSFNSGPQAALLDVASIAADKILLLDAYFSVVVFHGMTISQWRNMGYHHQ
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                VDMGKLLHAPMFGGYVQQGEAMLGLAMFREMGYSGFALDSVVMHGKSVHGWCIRRCSC
                LGLNLGNAITDMYVKCSILDYAHTVFVNMSRRDVISWSSLILGYGLDGDVVMSFKLFD
                EMLKEGIEPNAVTFLGVLSACAHGGLVEKSWLYFRLMOEYNIVPELKHYASVADCMSR
                AGLLEEAEKFLEDMPVKPDEAVMGAVLSGCKVYGNVEVGERVARELIQLKPRKASYYV
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                FGVLMSCENININSHIRDKEALVCQLVEGLQLPSEEIRGEILFALYKFSALQFTEQNV
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                TPSFGETADVLTSLQESLRHSILASLSLPEKDSTQILHAVYLLNEVYVYCTASTSINK
                {\tt TICIELRHCVIDVCTSHLLPWFLSDVNEVNEEATLGIMETFHSILLQNSDIQAKEFAE}
                \verb|LLVSADWFSFSFGCLGNFCTDNMKQRIYLMLSSLVDILLEQKTGSHIRDALHCLPSDP|
                QDLLFLLGQASSNNQELASCQSAALLIFHTSSIYNDRSLQNERYQISYSLEAERIIFH
                LLNEYEWDLGSINIHLESLKWLFQQESISKSLIYQIQKISRNNLIGNEVHNVYGDGRQ
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                NLSMNGIGSVIHRLVSGFSNSSLGTSFRTLLLLVFNILTSVQPAVLMIDESWYAVSIK
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                {\tt DVACSKGPALTQCQDETNIGEALAFTLLLYFFSLRSLQIVLAGAVD{\tt WQTFFGTSTSLE}}
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                MKAVLGGLVFCDDIRVATNSALCLSMILGWEDMEGRTEMLKTSSWYRFIAEEMSVSLA
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                VILFRELMQAELLNSQQVTKLDRAFQECRKQMHRNGTRDETVEEQVQRKIPSIHDHSE
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                EWNSPAKYPVDLKREEKKVKGRPFWVPFVCCSNEDGDWSKDHFWAVIRFLRQSSRLHE
                ILPNMKMTFCFFFQLQVFDTWKNLEPSRISENNYERIIRFLCEEKSMSEAIRAFRSMI
                DDHELSPSLEIYNSIIHSYADDGKFEEAMFYLNHMKENGLLPITETYDGLIEAYGKWK
                {\tt MYDEIVLCLKRMESDGCVRDHVTYNLLIREFSRGGLLKRMEQMYQSLMSRKMTLEPST}
                LLSMLEAYAEFGLIEKMEETCNKIIRFGISLDEGLVRKLANVYIENLMFSRLDDLGRG
                ISASRTRRTELAWCLRLLCHARLVSRKGLDYVVKEMEEARVPWNTTFANIALLAYSKM
                GDFTSIELLLSELRIKHVKLDLVTVGIVFDLSEARFDGTGVFMTWKKIGFLDKPVEMK
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exon
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                EVESASENRQGAQHSTEGHSMSSETVIESSQEAQVIDGGDTISNDRLETECKGKLTKE
                SQSKLASALGKREDTSDSSWNDEVIYSDVEGPYGFSSEATSMTHPDEASCIVSEDVPV
                {\tt HTSPVKADATQVISASKSVPDDMPFVENADVYLHGIKGFEEFEVSHSVNPFLPETSKG}
                EECEIDTLTEAENLGIKPEGLSIGSEVSSSDKLLAGDKTEPQGQTDLVAVKEFPSAEN
                ILISKINSEDIGMKAEEGKSSLGNAQTVESETLRVSLPAVDSVVVDSNADMSSAANKT
                GLVDLAGNESELMQANVVAEKGNKPKDTLSSESSCYASPVSVVFEGSDASDQIKSSTE
                TSKDSALQISAESKDEVCRESNNGRLVEESSFINEPNKTEYPISHFGSTGTAPDTVNT
                ANQTSLEIGRTE FNRVVGGLGVIQANEVDGNVKAHNNYAEVPVTIESNDHRDFGRLQN
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                 152089..152177, 152273..152405, 152494..152661))
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                 152089..152177, 152273..152405, 152494..152661))
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                /note="this enzyme converts phytoene into zeta-carotene
                via the intermediary of phytofluene by the symmetrical
                introduction of two double bonds at the c-11 and c-11'
                positions of phytoene
                EC_number=1.3.-.-"
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                /db xref="GOA:Q07356"
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                RTRRRSTAGPLQVVCVDIPRPELENTVNFLEAASLSASFRSAPRPAKPLKVVIAGAGL
                AGLSTAKYLADAGHKPLLLEARDVLGGKIAAWKDEDGDWYETGLHIFFGAYPNVQNLF
                GELGINDRLQWKEHSMI FAMPSKPGEFSRFDFPDVLPAPLNGIWAILRNNEMLTWPEK
                IKFAIGLLPAMVGGQAYVEAQDGLSVKEWMEKQGVPERVTDEVFIAMSKALNFINPDE
                {	t LSMQCILIALNRFLQEKHGSKMAFLDGNPPERLCMPVVDHIRSLGGEVQLNSRIKKIE}
                LNDDGTVKSFLLTNGSTVEGDAYVFAAPVDILKLLLPDPWKEIPYFKKLDKLVGVPVI
                NVHIWFDRKLKNTYDHLLFSRSNLLSVYADMSLTCKEYYDPNRSMLELVFAPAEEWIS
                RTDSDIIDATMKELEKLFPDEISADQSKAKILKYHVVKTPRSVYKTIPNCEPCRPLQR
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                 /protein_id="CAB46003.1"
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                {\tt RRRDGQISSSLVSSSDPTTIHPTDLVNLYRLSAISHVEHQNSNPCPSPGSMTPSPVSG}
                HSSIPADSNNGSRISPGPSPSRSSQSPKSPEASSLPEAIKSKLAAASAKYKESISKSK
                QGLKEKLLARNNSVKELSKGVQREMNAGIAGVARMIERMDFSSKRFGGSAHVSTSTAT
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                 /note="similar to R04E5.2 in Caenorhabditis elegans cosmid
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                 /product="hypothetical protein"
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                 /db xref="UniProt/TrEMBL:023281"
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                 VLFAGIMSGLTLGLMSLGLVELEILQRSGTPKEKKQSAAIFPVVQKQHQLLVTLLLFN
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                 VLGHNDPLFRRAQLKALVSIHGEAAGKGGELTHDETTIISGALDLTEKTAQEAMTPIE
                 STFSLDVNSKLDRVPANMPLYDILNEFQKGSSHMAAVVKVKGKSKGHPSTLHEENSGE
                 SNVSSNNSELTAPLLLKREGNHDSVIVRIDKANGQSFISEAGRQGFSHTSEEIEDGDE
                 EIVDETDEYIDVHKRIRVATVAAVAISSLARAPSGRRLLGPKGSGGPKTPKASSTPKP
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                 163974..164045,164162..164245,164312..164470,
                 164579..164662,164757..164833,164919..165165))
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                 164579..164662,164757..164833,164919..165165))
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                 /db xref="UniProt/TrEMBL:023282"
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                LVLFAGIMSGLTLGLMSLGLVELEILQRSGTPNEKKQAAAIFPVVQKQHQLLVTLLLC
                NAMAMEGLPIYLDKLFNEYVAIILSVTFVLAYGEVIPQAICTRYGLAVGANFVWLVRI
                LMTLCYPIAFPIGKVNIVCLVKNVLECSLILDLVLGHNDALFRRAQLKALVSIHSQEA
                GKGGELTHDETTIISGALDLTEKTAQEAMTPIESTFSLDVNSKLDWEAMGKILARGHS
                RVPVYSGNPKNVIGLLLVMLLTLILHVSMVAYHVSANSNQEIVLFSRVPADMPLYDIL
                NEFQKGSSHMAAVVKVKGKSKVPPSTLLEEHTDESNDSDLTAPLLLKREGNHDNVIVT
                IDKANGQSFFQNNESGPHGFSHTSEAIEDGEVIGIITLEDVFEELLQEEIVDETDEYV
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                complement (162861..162933)
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exon
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ESDSRLSSLYRPPPSLFFHGSFEDAKATSSREDLWLLVYDDTSEGQKISTFYKIDSVP
PVVLLIDPITGQKMRMWSGVIEPQGFLEDLMKYMDSGPHEHVASLTSNKRMKTEKISC
SSNNADDQDMATFWGNAIEEEKTVIKSGKEETFTSDRVVAPSWGPEFEDIMTLSEHEE
ETCLSCDLLEFPVLTEEPKADCDRSVVCSICVRFPDGRRKQRKFLKSEPIQLLWSFCY
SHMEESEKKEFKLVQAIPGASKTLDYGAKATFVQSGIANSMISVTWDINLPLDSKKTV
LSGCRVMIGQIASSGLTKKLMIKRNMWAKVRGVAMMNPVEHPHGGRTELGSHILNRDV
WANDAVSRTIESHFIVWQVYDDTNEGQKISSFYKIEAPPPVVFVINPITGOKMHMWSG
VIEAESIVEDLMMFWDAGPHENIASLTRNRRTETAETCLSSYNFYETPAPSWGEEFEE
EDNWSSRSNNNQVVAPTWEKELEEQDEWEIWSSRSDTDDFVPPFMGDEYEDPDEVKEE
EICLVFPVLTEEPKGDCDRSVVCSLCVRFPDGRRKQRKFLKSEPIQLLWSFCYSHIDE
SEKKAFKLVQAIPGASKTLDCEADATFDQSGLANSLISVTWE"
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175002..175484,176327..176653))
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translation="MDPPSDDAIISSNSSSITEKSSPPRNSFSELALSQKSRNHFEVV/
TRSHHFGEKSSTSRNSTGSNTGAFGFSVDNLRSIVAVIFHLKLTLKQSQKLRNSNRFI
VMKSEIRRHKNVVRMFSSTTSHTSGWDSDDETKVTQLLSSEPAYPFLLIEYITNIQNS
SSDGRVIVYDDDSSKGKATKVTIKDKKLEKEVIEAMTVGFLRDGLKFYLSYRSSDHQP
VITYETSNPKLENLTIHLPSVPTGTKIHNLAMSSIPVQDKDWVVGVKLSGSRCINPLS
SLMFSKRDQRFYIPSYGGNYLCYLDLNSKEGDDHFNSRQENGQPSFIDLDYENLPESV
FKQLAGVSSCSKTDHLVESPTGQLFLVKWFVEDVEDLCDNTPMHVTKKFMVFRANEAS
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exon

intron

exon

intron

exon

intron

gene

gene

CDS

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                DDFSVMEEEFEEMIASSDGGSMADTVTEADVASYLKMLLNIAESTKEKIYRSKVSSCS
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                NDGKCWKFCLMVAKSGVLCIGSIQIDGQKHTAPWIPEDNSICCKEHPSVGRCLPNIDD
                SAEKGGKCWKFCIEGCETGGFCKLFGHKHICHCNCSG"
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                /product="hypothetical protein"
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                FSRSHELELQHQSKYTISGINIFRFLVKQINQIFHQVAHIAGDDNRPSVRETRTVQRN
                SGHITRTRTWKSSDVPMLPYTGWVFVSRNVSRIFYWLQIASAFASIFISTIQLIKQDY
                GGNDLKPKSTNLHAALTLFYSLALAEALLFLVEKAYWEYMISVIHILEKVNEECGLER
                FGTGSVRRFFYDAYSRCLNGSIFDGLKMDMVIFAMELLVANSLDEQLIGAEILSIFST
                HDDYSVDTLQKIGTNLAIIERLVEMLNWRDKNQEDVRMSAAEILSRLASKKONSLRVA
                GIPGAIESISSLLESTRDSGEATDEIGEQSINHSNLWTLNNLGLLILKRLARDHENCG
                KIGKTKGLLSKIIDFTYAEKNLLENPNVAVAEPYKILAVKRSLKLLKKLVSTTGTTGK
                NLRMTISGIVFTVSNIRETLHHGKSQPHLQKLGAEILTFLAFEEGATEKIGGTGGVLK
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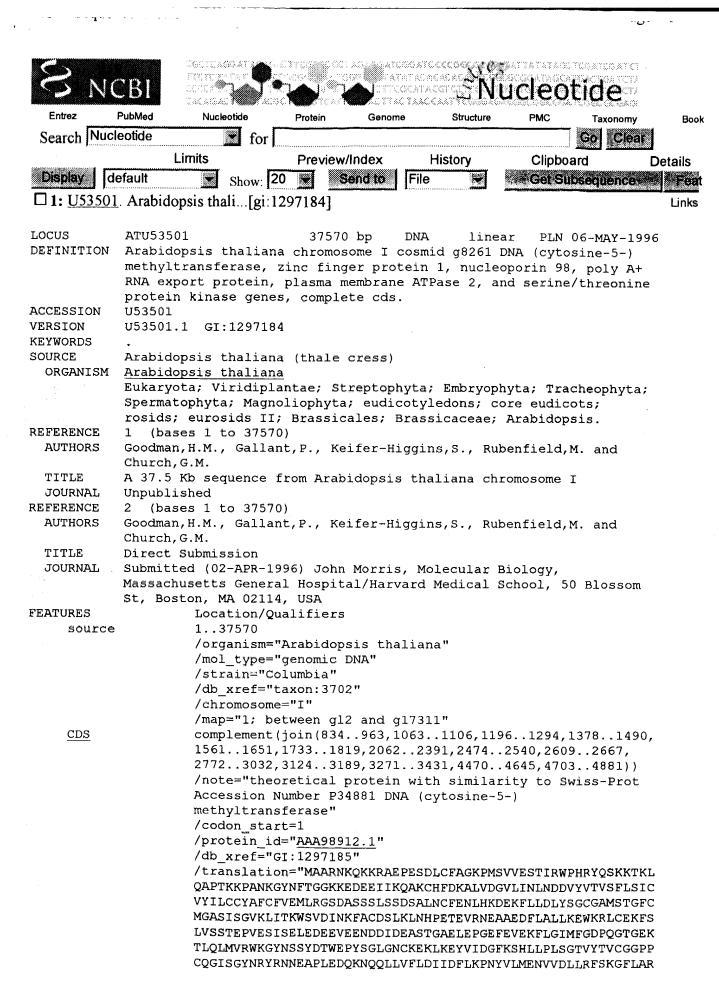
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Oct 4 2004 14:35:49



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